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1653

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/509,994

DATE: 11/08/2001

TIME: 12:22:23

Input Set : A:\Kp-8753.app

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3 <110> APPLICANT: YUI, MASAKI
4 YOKOZAWA, AKIRA
5 MURATA, TOMOYO
6 TSURUTA, KAZUHISA
7 SHIMIZU, HIROTOMO
9 <120> TITLE OF INVENTION: METHOD FOR KEEPING THE QUALITY OF AQUEOUS PARENTERAL
10 SOLUTION OF THROMBOMODULIN IN STORAGE AND DISTRIBUTION
12 <130> FILE REFERENCE: KP-8753
14 <140> CURRENT APPLICATION NUMBER: 09/509,994
15 <141> CURRENT FILING DATE: 2000-05-08
17 <150> PRIOR APPLICATION NUMBER: PCT/JP98/04609
18 <151> PRIOR FILING DATE: 1998-10-13
20 <150> PRIOR APPLICATION NUMBER: JP 9-281659
21 <151> PRIOR FILING DATE: 1997-10-15
23 <150> PRIOR APPLICATION NUMBER: JP 9-308523
24 <151> PRIOR FILING DATE: 1997-11-11
26 <160> NUMBER OF SEQ ID NOS: 6
28 <170> SOFTWARE: PatentIn Ver. 2.1
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 516
32 <212> TYPE: PRT
33 <213> ORGANISM: Homo sapiens
35 <220> FEATURE:
36 <223> OTHER INFORMATION: Partial amino acid sequences of a human
37 thrombomodulin
39 <400> SEQUENCE: 1
40 Met Leu Gly Val Leu Val Leu Gly Ala Leu Ala Leu Ala Gly Leu Gly
41 1 5 10 15
43 Phe Pro Ala Pro Ala Glu Pro Gln Pro Gly Gly Ser Gln Cys Val Glu
44 20 25 30
46 His Asp Cys Phe Ala Leu Tyr Pro Gly Pro Ala Thr Phe Leu Asn Ala
47 35 40 45
49 Ser Gln Ile Cys Asp Gly Leu Arg Gly His Leu Met Thr Val Arg Ser
50 50 55 60
52 Ser Val Ala Ala Asp Val Ile Ser Leu Leu Leu Asn Gly Asp Gly Gly
53 65 70 75 80
55 Val Gly Arg Arg Arg Leu Trp Ile Gly Leu Gln Leu Pro Pro Gly Cys
56 85 90 95
58 Gly Asp Pro Lys Arg Leu Gly Pro Leu Arg Gly Phe Gln Trp Val Thr
59 100 105 110
61 Gly Asp Asn Asn Thr Ser Tyr Ser Arg Trp Ala Arg Leu Asp Leu Asn
62 115 120 125
64 Gly Ala Pro Leu Cys Gly Pro Leu Cys Val Ala Val Ser Ala Ala Glu
65 130 135 140
67 Ala Thr Val Pro Ser Glu Pro Ile Trp Glu Glu Gln Gln Cys Glu Val
68 145 150 155 160
70 Lys Ala Asp Gly Phe Leu Cys Glu Phe His Phe Pro Ala Thr Cys Arg

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71                               165                               170                               175
73 Pro Leu Ala Val Glu Pro Gly Ala Ala Ala Val Ser Ile Thr
74                               180                               185                               190
76 Tyr Gly Thr Pro Phe Ala Ala Arg Gly Ala Asp Phe Gln Ala Leu Pro
77                               195                               200                               205
79 Val Gly Ser Ser Ala Ala Val Ala Pro Leu Gly Leu Gln Leu Met Cys
80                               210                               215                               220
82 Thr Ala Pro Pro Gly Ala Val Gln Gly His Trp Ala Arg Glu Ala Pro
83 225                               230                               235                               240
85 Gly Ala Trp Asp Cys Ser Val Glu Asn Gly Gly Cys Glu His Ala Cys
86                               245                               250                               255
88 Asn Ala Ile Pro Gly Ala Pro Arg Cys Gln Cys Pro Ala Gly Ala Ala
89                               260                               265                               270
91 Leu Gln Ala Asp Gly Arg Ser Cys Thr Ala Ser Ala Thr Gln Ser Cys
92                               275                               280                               285
94 Asn Asp Leu Cys Glu His Phe Cys Val Pro Asn Pro Asp Gln Pro Gly
95                               290                               295                               300
97 Ser Tyr Ser Cys Met Cys Glu Thr Gly Tyr Arg Leu Ala Ala Asp Gln
98 305                               310                               315                               320
100 His Arg Cys Glu Asp Val Asp Asp Cys Ile Leu Glu Pro Ser Pro Cys
101                               325                               330                               335
103 Pro Gln Arg Cys Val Asn Thr Gln Gly Gly Phe Glu Cys His Cys Tyr
104                               340                               345                               350
106 Pro Asn Tyr Asp Leu Val Asp Gly Glu Cys Val Glu Pro Val Asp Pro
107                               355                               360                               365
109 Cys Phe Arg Ala Asn Cys Glu Tyr Gln Cys Gln Pro Leu Asn Gln Thr
110                               370                               375                               380
112 Ser Tyr Leu Cys Val Cys Ala Glu Gly Phe Ala Pro Ile Pro His Glu
113 385                               390                               395                               400
115 Pro His Arg Cys Gln Met Phe Cys Asn Gln Thr Ala Cys Pro Ala Asp
116                               405                               410                               415
118 Cys Asp Pro Asn Thr Gln Ala Ser Cys Glu Cys Pro Glu Gly Tyr Ile
119                               420                               425                               430
121 Leu Asp Asp Gly Phe Ile Cys Thr Asp Ile Asp Glu Cys Glu Asn Gly
122                               435                               440                               445
124 Gly Phe Cys Ser Gly Val Cys His Asn Leu Pro Gly Thr Phe Glu Cys
125                               450                               455                               460
127 Ile Cys Gly Pro Asp Ser Ala Leu Val Arg His Ile Gly Thr Asp Cys
128 465                               470                               475                               480
130 Asp Ser Gly Lys Val Asp Gly Gly Asp Ser Gly Ser Gly Glu Pro Pro
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137                               515
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141 <211> LENGTH: 516
142 <212> TYPE: PRT
143 <213> ORGANISM: Homo sapiens

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145 &lt;220&gt; FEATURE:

146 <223> OTHER INFORMATION: Partial amino acid sequences of a human  
147 thrombomodulin

149 &lt;400&gt; SEQUENCE: 2

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150 Met Leu Gly Val Leu Val Leu Gly Ala Leu Ala Leu Ala Gly Leu Gly
151   1           5           10           15
153 Phe Pro Ala Pro Ala Glu Pro Gln Pro Gly Gly Ser Gln Cys Val Glu
154           20           25           30
156 His Asp Cys Phe Ala Leu Tyr Pro Gly Pro Ala Thr Phe Leu Asn Ala
157           35           40           45
159 Ser Gln Ile Cys Asp Gly Leu Arg Gly His Leu Met Thr Val Arg Ser
160           50           55           60
162 Ser Val Ala Ala Asp Val Ile Ser Leu Leu Leu Asn Gly Asp Gly Gly
163   65           70           75           80
165 Val Gly Arg Arg Arg Leu Trp Ile Gly Leu Gln Leu Pro Pro Gly Cys
166           85           90           95
168 Gly Asp Pro Lys Arg Leu Gly Pro Leu Arg Gly Phe Gln Trp Val Thr
169           100          105          110
171 Gly Asp Asn Asn Thr Ser Tyr Ser Arg Trp Ala Arg Leu Asp Leu Asn
172           115          120          125
174 Gly Ala Pro Leu Cys Gly Pro Leu Cys Val Ala Val Ser Ala Ala Glu
175           130          135          140
177 Ala Thr Val Pro Ser Glu Pro Ile Trp Glu Glu Gln Gln Cys Glu Val
178   145          150          155          160
180 Lys Ala Asp Gly Phe Leu Cys Glu Phe His Phe Pro Ala Thr Cys Arg
181           165          170          175
183 Pro Leu Ala Val Glu Pro Gly Ala Ala Ala Ala Val Ser Ile Thr
184           180          185          190
186 Tyr Gly Thr Pro Phe Ala Ala Arg Gly Ala Asp Phe Glu Ala Leu Pro
187           195          200          205
189 Val Gly Ser Ser Ala Ala Val Ala Pro Leu Gly Leu Gln Leu Met Cys
190           210          215          220
192 Thr Ala Pro Pro Gly Ala Val Gln Gly His Trp Ala Arg Glu Ala Pro
193   225          230          235          240
195 Gly Ala Trp Asp Cys Ser Val Glu Asn Gly Gly Cys Glu His Ala Cys
196           245          250          255
198 Asn Ala Ile Pro Gly Ala Pro Arg Cys Gln Cys Pro Ala Gly Ala Ala
199           260          265          270
201 Leu Gln Ala Asp Gly Arg Ser Cys Thr Ala Ser Ala Thr Gln Ser Cys
202           275          280          285
204 Asn Asp Leu Cys Glu His Phe Cys Val Pro Asn Pro Asp Gln Pro Gly
205           290          295          300
207 Ser Tyr Ser Cys Met Cys Glu Thr Gly Tyr Arg Leu Ala Ala Asp Gln
208   305          310          315          320
210 His Arg Cys Glu Asp Val Asp Asp Cys Ile Leu Glu Pro Ser Pro Cys
211           325          330          335
213 Pro Gln Arg Cys Val Asn Thr Gln Gly Gly Phe Glu Cys His Cys Tyr
214           340          345          350
216 Pro Asn Tyr Asp Leu Val Asp Gly Glu Cys Val Glu Pro Val Asp Pro

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217          355          360          365
219 Cys Phe Arg Ala Asn Cys Glu Tyr Gln Cys Gln Pro Leu Asn Gln Thr
220          370          375          380
222 Ser Tyr Leu Cys Val Cys Ala Glu Gly Phe Ala Pro Ile Pro His Glu
223 385          390          395          400
225 Pro His Arg Cys Gln Met Phe Cys Asn Gln Thr Ala Cys Pro Ala Asp
226          405          410          415
228 Cys Asp Pro Asn Thr Gln Ala Ser Cys Glu Cys Pro Glu Gly Tyr Ile
229          420          425          430
231 Leu Asp Asp Gly Phe Ile Cys Thr Asp Ile Asp Glu Cys Glu Asn Gly
232          435          440          445
234 Gly Phe Cys Ser Gly Val Cys His Asn Leu Pro Gly Thr Phe Glu Cys
235          450          455          460
237 Ile Cys Gly Pro Asp Ser Ala Leu Ala Arg His Ile Gly Thr Asp Cys
238 465          470          475          480
240 Asp Ser Gly Lys Val Asp Gly Gly Asp Ser Gly Ser Gly Glu Pro Pro
241          485          490          495
243 Pro Ser Pro Thr Pro Gly Ser Thr Leu Thr Pro Pro Ala Val Gly Leu
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251 <211> LENGTH: 1548
252 <212> TYPE: DNA
253 <213> ORGANISM: Homo sapiens
255 <220> FEATURE:
256 <223> OTHER INFORMATION: Partial base sequences of a human thrombomodulin
257 gene
259 <400> SEQUENCE: 3
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262 ggcccgcgga ccttctctca tgcacgtcag atctgcgacg gactgcgggg ccacctaatg 180
263 acagtgcgct cctcggtggc tgcgcgatgc atttctctgc tactgaacgg cgacggcgcg 240
264 gttggccgcc ggcgcctctg gatcgccctg cagctgccac ccggctgcgg cgaccccaag 300
265 cgctcggggc cctcgcgcgg ctctccagtg gttacgggag acaacaacac cagctatagc 360
266 aggtggggac ggctcgacct caatggggct cccctctgcg gccctgtgtg cgtcgtctgc 420
267 tccgctgtct aggccactgt gccacgcgag cgcactctgg aggacagcca gtgcgaagtg 480
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271 cagctaattg gcaccgcgcc gcccgagcgg gtccaggggg actggggcag ggagcgcgcg 720
272 ggcgcttggg actgcagcgt ggagaacggc ggctgcgagc acgcgtgcga cgtgatccct 780
273 ggggctcccc gctgccagtg cccagccggc gccgcctcgg aggcagacgg gcgctctcgc 840
274 accgcatccg cgacgcagtc ctgcgaacgc ctctgcgagc acttctgcgt tcccaacccc 900
275 gaccagccgg gctcctactc gtgcagtgtg gagaccggct accggcttgc ggccgaccaa 960
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278 gagtgtgtgg agcccggtga cccgtgcttc agagccaact gcgagtacca gtgccagccc 1140
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283 accttcgagt gcatctcggt gcccgactcg gcccttgtcc gccacattgg caccgactgt 1440
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289 <211> LENGTH: 1548
290 <212> TYPE: DNA
291 <213> ORGANISM: Homo sapiens
293 <220> FEATURE:
294 <223> OTHER INFORMATION: Partial base sequences of a human thrombomodulin
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297 <400> SEQUENCE: 4
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300 ggccccgcga cttctccaa tgccagtcag atctgcgacg gactgcgggg ccacctaatg 180
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322 gactccgca aggtggaagg tggcgacagc ggctctggcg agcccccgcc cagcccgaag 1500
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332 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
333     peptide
335 <220> FEATURE:
336 <223> OTHER INFORMATION: Synthetic DNA for mutation

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VERIFICATION SUMMARY

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